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A habitat quality indicator for common birds in Europe based on species distribution models

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A B S T R A C T

The EU 2020 Biodiversity Strategy requires the gathering of information on biodiversity to aid in monitoring progress towards its main targets. Common species are good proxies for the diversity and integrity of ecosystems, since they are key elements of the biomass, structure, functioning of ecosystems, and therefore of the supply of ecosystem services. In this sense, we aimed to develop a spatially-explicit indicator of habitat quality (HQI) at European level based on the species included in the European Common Bird Index, also grouped into their major habitat types (farmland and forest). Using species occurrences from the European Breeding Birds Atlas (at 50 km × 50 km) and the maximum entropy algorithm, we derived species distribution maps using refined occurrence data based on species ecology. This allowed us to cope with the limitations arising from modelling common and widespread species, obtaining habitat suitability maps for each species at finer spatial resolution (10 km × 10 km grid), which provided higher model accuracy. Analysis of the spatial patterns of local and relative species richness (defined as the ratio between species richness in a given location and the average richness in the regional context) for the common birds analysed demonstrated that the development of a HQI based on species richness needs to account for the regional species pool in order to make objective comparisons between regions. In this way, we proved that relative species richness compensated for the bias caused by the inherent heterogeneous patterns of the species distributions that was yielding larger local species richness in areas where most of the target species have the core of their distribution range. The method presented in this study provides a robust and innovative indicator of habitat quality which can be used to make comparisons between regions at the European scale, and therefore potentially applied to measure progress towards the EU Biodiversity Strategy targets. Finally, since species distribution models are based on breeding birds, the HQI can be also interpreted as a measure of the capacity of ecosystems to provide and maintain nursery/reproductive habitats for terrestrial species, a key maintenance and regulation ecosystem service.

1. Introduction

The EU 2020 Biodiversity Strategy has as headline target to halt the loss of biodiversity and degradation of ecosystem services in the EU by 2020. The Strategy therefore calls for the gathering of comprehensive information on the status of biodiversity, ecosystems and ecosystem services and the development of coherent and robust indicators to monitor, assess and report on progress in its implementation across the EU.

The Streamlining European Biodiversity Indicators (SEBI) have been set to address the EU Biodiversity Targets (EEA, 2012). The 'abundance and distribution of selected species' (SEBI 01) is among these indicators and includes, among other groups, common birds. Common species contribute to much of the structure, biomass and energy turnover of an ecosystem, so are a determinant of ecosystem function, with the depletion of their population potentially affecting ecosystem goods and services in a significant way (McIntyre et al., 2007; Gaston and Fuller, 2008; Gaston, 2010). Moreover, birds are considered to be good proxies to measure the diversity and integrity of ecosystems as they tend to be near the top of the

Abbreviations: AUC, Area Under the receiver operating characteristic Curve; EBCC, European Bird Census Council; HQI, habitat quality indicator; LUISA, Land Use-based Integrated Sustainability Assessment modelling platform; LSR, local species richness; NM_{AUC}, null model AUC; RSR, relative species richness; SDM, species distribution models; SM_{AUC}, species model AUC; SEBI, Streamlining European Biodiversity Indicators.

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food chain, have large ranges, and the ability to move elsewhere when their environment becomes unsuitable (Sekercioglu, 2006). The abundance of common birds is currently reported by the European Common Bird Index (Gregory et al., 2005; Eurostat, 2013). The negative population trends described by this indicator during recent years, particularly for farmland birds, reveal an increasing threat to those species within certain habitat types (Eurostat, 2013).

A great deal of work has been done to include data on species abundance and population trends of common birds within the framework of the SEBI 01 indicator (Inger et al., 2014), with much less of a focus on the spatial distribution of selected species. There is, therefore, a need to evaluate the spatial distribution patterns at European level of the species included in the Common Bird Index. In spite of the great usefulness of species distribution models (SDM) to map habitat suitability of species at large spatial scales (Araujo et al., 2005; Elith et al., 2011; Virkkala et al., 2013; Thuiller et al., 2014), there are, as yet, no published studies on modelling the distribution of the species listed in the widely accepted European Common Bird Index. Species distribution maps obtained through SDM indicate the probability of presence of a given species based on the spatial variation of environmental conditions. A higher probability of presence of a modelled species can be considered an indicator of habitat quality (Sergio and Newton, 2003) that will be useful to identify areas offering good habitat conditions for all the target species. Computing and overlaying the SDM for the common bird species therefore offers a unique opportunity to develop a composite indicator on the habitat quality of this group of species.

However, when assessing the species richness derived from the SDM outputs for a set of target species over a broad spatial extent, there may be an influence of the dominant distribution patterns depending on the biogeography of the species selected for the analysis. A higher species richness is expected closer to areas where most of the species have the core of distribution range, where individual species are more homogeneously distributed, and there is an increased likelihood of overlap with other species (Soberón and Ceballos, 2011). On the contrary, towards the periphery of the distribution ranges, species appear in more isolated and fragmented patches decreasing the probability of overlay, and potentially yielding lower species richness. If this hypothesis holds, the use of local species richness as an indicator would result in a biased comparison between regions, overestimating the role of species richness in those areas closer to the core ranges of the species analysed. Therefore, the indicator might be highly variable depending on the species selected and the specific location considered for the analysis.

Spatial variation in local species richness may not only be linked to variations in local environmental conditions, but also to the size of the regional species pool. Using relative species richness (RSR), expressed as local species richness in relation to the regional species pool, should help to resolve this issue (Cam et al., 2000). Relative species richness should then be independent of the geographic position in relation to the core or periphery range of the studied species, which would warrant its use as a robust indicator of habitat quality for common birds.

In this context, the general objective of this study was to develop a habitat quality indicator (HQI) based on the richness of species included in the European Common Bird Index, also grouped into major habitat types (farmland and forest). Species richness was obtained from species distribution models (SDM) using occurrence data refined according to the species ecology, allowing us to obtain downscaled habitat suitability maps. Finally, we analysed the spatial patterns of local and relative species richness throughout Europe to test the influence of the dominant pattern of species distributions, as explained above. This analysis would prove the soundness of using species richness, either local or relative, as a spatial indicator of habitat quality, allowing us to make objective comparisons between regions as required for appropriate environmental indicators (OECD, 1993; EEA, 2012).

2. Methods

2.1. Bird species data and refined species occurrences

Presence-only data on bird species occurrences were obtained from the European Bird Census Council (EBCC) Atlas of European Breeding Birds, over a grid of roughly 50 km × 50 km (Hagemeijer and Blair, 1997). Of the 148 species included in the Common Bird Index (Appendix A) (European Bird Census Council, Species classification 2012), only data on the Syrian woodpecker (*Dendrocopos syriacus*) was not available in the EBCC Atlas. A given species was considered to be breeding when a record was classified as 'confirmed breeding' (i.e. Category C from the EBCC Atlas). Species of the Common Bird Index are classified according to habitat types in Europe and include 37 farmland species, 33 forest species and a very heterogeneous group of 78 species found in other habitat types (i.e. urban, water, generalist birds). Following the Common Bird Index, we present results for all common bird species (including all three groups) and then separately for farmland and forest common birds.

The modelling of widespread and common species is challenging since these species do not show strong responses to environmental gradients leading, in some cases, to poor model performance (McPherson et al., 2004; Segurado and Araújo, 2004; Franklin et al., 2009; Aguirre-Gutiérrez et al., 2013). In fact, a large distribution range in relation to the modelled extent might result in low discriminatory power between areas where the species is present or absent (Franklin et al., 2009; Aguirre-Gutiérrez et al., 2013). Keeping the original resolution of the Atlas data we expected to face this issue for about 52% of the targeted species, whose distribution ranges cover more than half the study area (i.e. Europe). The coarse spatial resolution of the EBCC Atlas data may also yield situations in which species show similar distribution ranges (and therefore very similar explanatory variables in their SDM), even when the species have contrasting habitat requirements. For instance, *Garrulus glandarius* and *Hirundo rustica* show a Jaccard's index of similarity of their EBCC occurrences of 0.85, but have completely different habitat requirements, belonging respectively to the farmland and forest species groups. In addition, SDM based on land use usually require a finer spatial resolution than those based solely on climate, given that land use is a much more heterogeneous factor than climate at the landscape scale (Kelly et al., 2014; Sohl, 2014).

The foregoing arguments justify the development of a suitable approach to refine the available species occurrence data to model species distributions for common birds. This would also contribute towards providing downscaled distribution models for a more detailed assessment of habitat quality for the target species, improving the applicability to support policy decisions. To achieve this refinement, 10 km × 10 km cells were randomly sampled within each occupied cell of the original EBCC Atlas presence-only data (∼ at 50 km × 50 km resolution). The sampling was constrained by species habitat preferences, so that only fine-grain cells for which the extent of the preferred habitat for each species is above the 50th percentile can be selected. The downscaling of coarse occurrence data based on species habitat preferences has also been done in other studies (McPherson et al., 2006; Rondinini et al., 2011; Sardà-Palomera and Vieites, 2011; Overmars et al., 2013). Habitat preferences for each species were taken from BirdLife International (2014), where suitable breeding habitats are listed using the IUCN habitat classification scheme (IUCN, 2012). We harmonized the IUCN habitats with the Corine Land Cover (CLC) classes (Appendix B) to calculate the proportion of suitable breeding habitats within the 10 km × 10 km grid cells of the European Environment Agency reference grid. Moderate levels of downscaling (i.e. 5-fold from

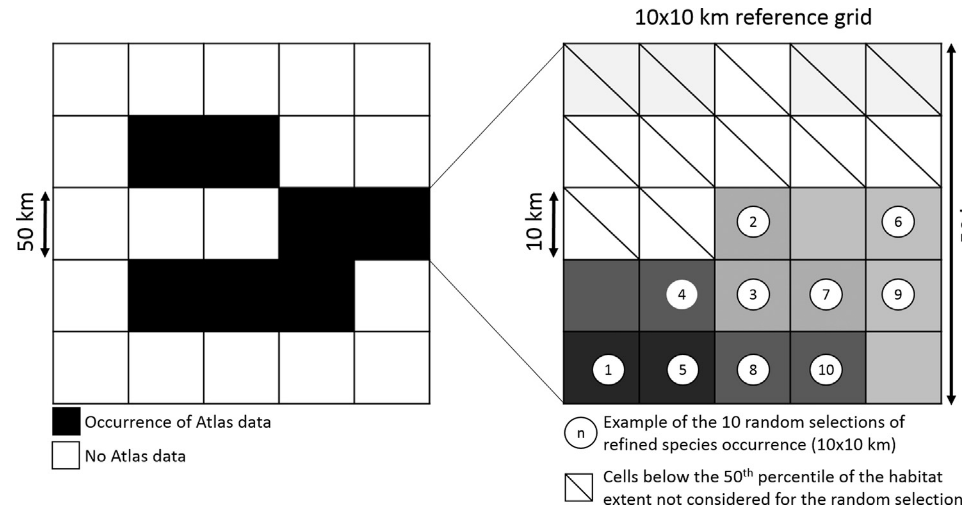

Fig. 1. Schematic representation of the random sampling of grid cells for the refinement of the EBCC Atlas species occurrence data, from ∼50 km × 50 km (on the left) to 10 km × 10 km (on the right). The greyscale used within the 10 × 10 grid indicates the increasing proportion of preferred habitat available for a given species; only cells with values above the 50th percentile can be randomly selected in the 10 repetitions.

Table 1
Environmental variables included as predictors in species distribution models.

Climate	Mean temperature of the coldest month Mean temperature of the warmest month Mean precipitation of the wettest month Mean precipitation of the driest month
Land uses (in %)	Artificial Arable Permanent crops Pastures Natural land Transitional woodland-shrub Forests Other nature Wetlands Water bodies
Miscellaneous	Distance to large artificial areas (squared) Simpson land use diversity

50 km × 50 km to 10 km × 10 km) have been shown to allow for reasonably accurate results when modelling species distribution, regardless of the technique used (Bombi and D'Amen, 2012). However, to increase robustness, we repeated the constrained random selection of fine-grain cells for each species 10 times, obtaining 10 different downscaled occurrences per species (Fig. 1).

With this approach, the same number of occurrences as in the original Atlas data should be maintained. However, for 13 species (mainly water birds such as *Tringa totanus* and *Motacilla cinerea*), occupied coarse-grain cells were not included in the analysis if breeding habitats (e.g. freshwater habitats) were not present in that cell, so slightly reducing the original number of occurrences by around 5%. This was done to reduce the bias in the modelled relationship between the occurrence and the land use data, since required breeding habitats might not be appropriately captured in the cartography at European level (i.e. CLC).

2.2. Environmental variables

We included the following predictors in the SDM: four climate variables from the Worldclim database (Hijmans et al., 2005); the proportion of ten land use classes within each grid cell; the Simpson land use diversity index, and the distance to artificial areas larger than 20 km^2 (Table 1). The selection of climate variables was based on previous studies (Thuiller et al., 2014), excluding temperature seasonality because of its high correlation with mean temperature of the coldest month (Pearson's correlation coefficient >0.80).

The land use classes were taken from an updated version of Corine Land Cover (CLC) 2000, roughly matching the bird sampling period of the EBCC Atlas (with most of the field work done between 1985 and 1988). The CLC map for 2000 was updated to make it directly comparable to the CLC 2006, obtaining as land use changes of their comparison those reported by the European Environment Agency. This will facilitate the projection of the models developed in this study on future land use scenarios. The original land-use classes were aggregated (Appendix C) according to the classification in use by the Land Use-based Integrated Sustainability Assessment modelling platform (LUISA) (Baranzelli et al., 2014). LUISA is currently employed within the European Commission to evaluate socio-economic and environmental impacts of European policies. Conformity to the LUISA land-use classification therefore allows us to fully integrate our indicator into the platform, and hence to assess how the indicator may change in response to different policies.

2.3. Species distribution models

We chose the maximum entropy method implemented in Maxent (Phillips et al., 2006) to model bird species distributions since this method has been shown to provide high predictive performance, especially for presence-only data (Elith et al., 2006; Aguirre-Gutiérrez et al., 2013).

We initially run the SDM using the original occurrences of the EBCC Atlas data (∼50 km × 50 km), followed by the 10 random replicates (samplings) per species refined at 10 km × 10 km. The Maxent models gives as output the probability of presence for each species, which were converted into binary 'presence/absence' maps using the '10 percentile of the training presences' as cut-off threshold (i.e. a presence is only registered if the probability of presence is greater than or equal to this value). To reduce uncertainty, we only considered that a given species was present in areas where all (10) binary maps obtained from the random replicates predicted a 'presence' (i.e. consensus presence). The consensus presence for a given species was then overlaid to give a summed species presence for all common birds, and also separately for farmland and forest common species. This value is indicative of species richness hotspots, where most of the target species meet their ecological requirements.

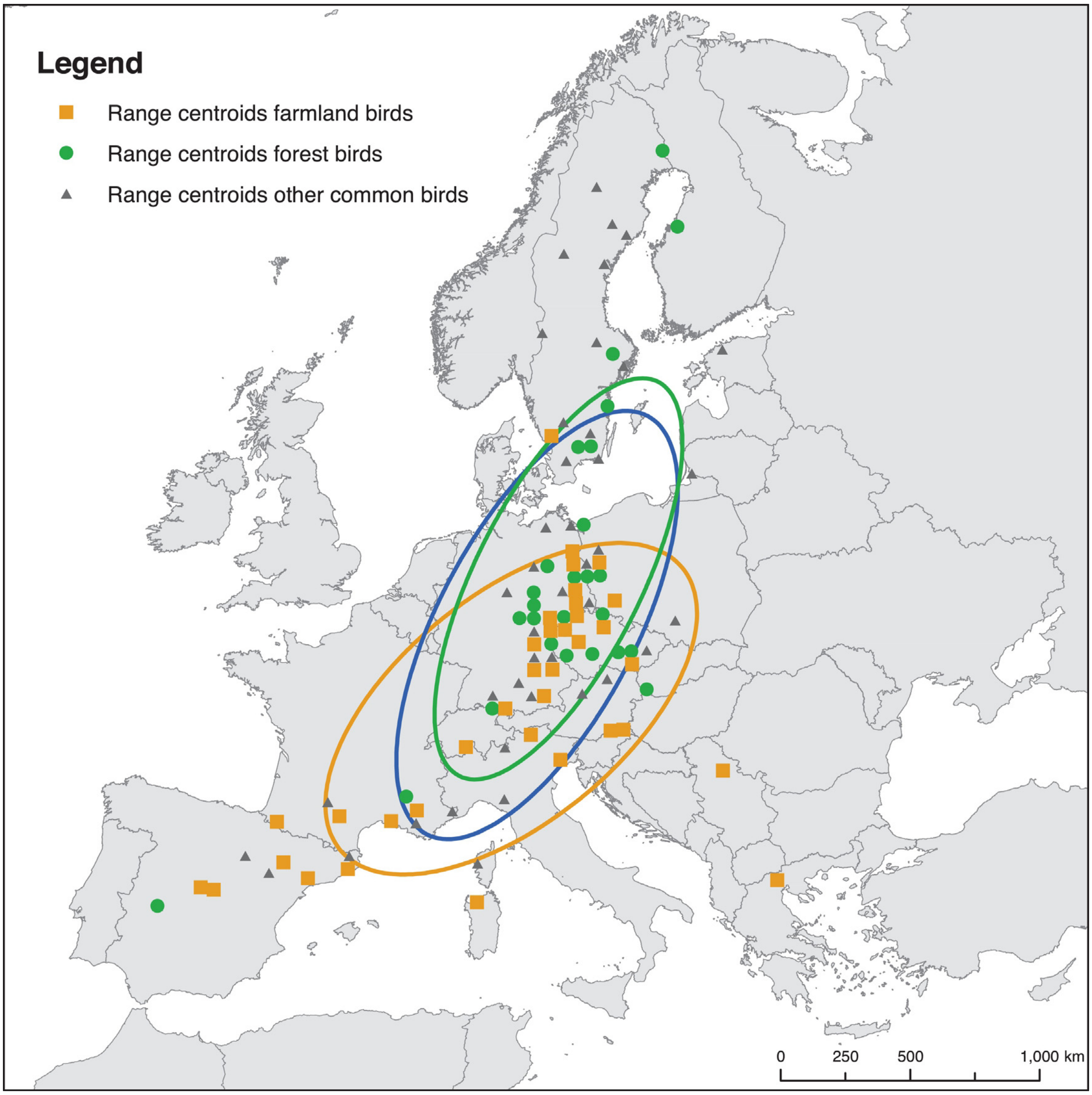

Fig. 2. Centroids of the distributional ranges for all common birds, grouped by farmland species (■), forest species (●), and species associated to other habitats (▲). Ellipses of the same respective colours summarise the spatial properties of the centroids (i.e. central tendency, dispersion, and directional trends) for farmland and forest species, being the blue one the ellipse for all common birds (■, ●, ▲). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

For each species, model performance at both 50 km × 50 km and 10 km × 10 km resolution was assessed by means of the Area Under the receiver operating characteristic Curve (AUC) and the omission rate (proportion of the test localities falling outside the prediction) for the '10 percentile of the training presences' threshold (Phillips et al., 2006). Both measurements of model performance were calculated using 70% of the data to train the model and the remaining 30% for model evaluation. For models run at 10 km × 10 km, we averaged the model performances over the 10 replicates. AUCs and omission rates obtained by the SDM at 50 km × 50 km and 10 km × 10 km were then compared by the non-parametric Wilcoxon signed-rank test.

Since models using presence-only data can only achieve a maximum AUC less than one (maximum AUC = 1 – area occupied/2, Wiley et al., 2003), we expected to obtain low discriminatory performance for some common and widespread species. Therefore, for species with AUC values below 0.75 (Elith, 2002), we built a set of null models (10 per species) to evaluate model performance in a complementary way. In null models, species occurrences are replaced by an equivalent number of randomly selected locations (Raes and ter Steege, 2007). The AUC obtained from these null models (NM_{AUC}) is taken as a threshold for evaluating model discriminatory power (Scott et al., 2002). Only when the average AUC values for the modelled species (SM_{AUC}) were significantly higher than the average NM_{AUC} (Student's *t*-test <0.05), was the species model retained for further analyses.

2.4. Analysis of spatial patterns of species richness

In this study, we calculated local species richness (LSR) as the summed individual species presence obtained from the downscaled SDM for common birds in Europe (i.e. all common, forest and farmland birds) at 10 km × 10 km grid cell resolution. In order to overcome the likely influence on species richness of spatial variation in the regional species pool (Cam et al., 2000), we also calculated relative species richness (RSR). RSR was calculated by dividing LSR for a given pixel by the average richness in a broad regional context (RSR = local species richness/average regional species richness). The average richness in the regional context reflects the potential species richness that might be found in

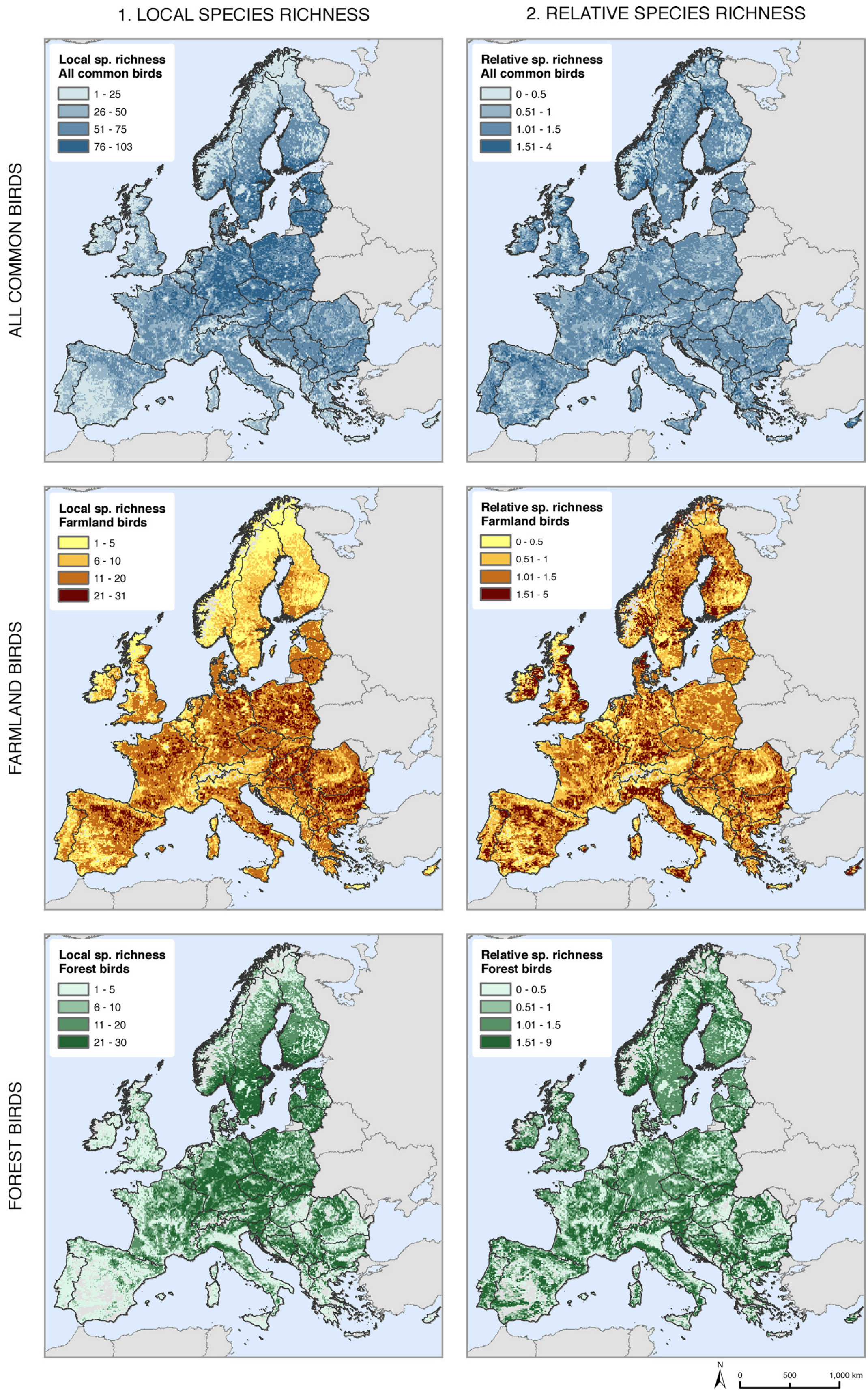

Fig. 3. Maps of (1) local species richness obtained from the overlay of species distribution models (SDM) of common birds in Europe and (2) relative species richness calculated as the ratio between local species richness and the average richness in the regional context. Results are given for all common birds in Europe, farmland birds and forest birds.

a given location according to the regional conditions. We used a 250 km radius to account for the regional context, which was considered large enough to represent the regional conditions.

We analysed the patterns of LSR and RSR for all common bird species, assessing also farmland and forest common birds separately, to test whether higher values were indeed found in locations closer to where most of the target species have the core of their distribution range. For this purpose, we defined the species range as the set of all its occurrences in the EBCC Atlas and calculated the centroid of these occurrences per species to indicate the core of its distribution. All species centroids were merged in a single layer to calculate the standard deviational ellipse that summarises the spatial characteristics of the analysed centroids (i.e. directional distribution tool in ArcGIS 10.2). This ellipse describes the dominant pattern of species ranges, by means of its location and dispersion (Fig. 2); the larger the ellipse, the more dispersed are the cores of species distributions. We then calculated throughout the whole study area the Euclidean distance to the dominant pattern of species distributions to test our hypothesis and analyse how LSR and RSR may change as a function of this distance.

We analysed the non-parametric correlation between LSR and RSR respectively, and the distance to the dominant pattern of species distributions for each group of species. Correlation analyses were performed by random subsampling of 100 observations 1000 times at 10 km × 10 km resolution taken from the full extent of the study area (Europe). Complementarily, we also analysed non-parametric correlation at the scale at which regional policies are usually applied in the European Union (i.e. nomenclature of territorial units for statistics, NUTS2 regions). Non-significant correlation would confirm the use of the local or relative species richness as proxies for the HQI, which should allow the comparison of habitat quality between locations without the influence of the distance to the dominant pattern of the distributions.

3. Results

3.1. Distribution models of common birds

The sum of species presence by functional group obtained from the SDM resulted in maps of LSR. These are shown for all common birds, and separately for farmland and forest common birds in Fig. 3(1). Especially for all common birds and forest birds, LSR shows main hotspots in central Europe, roughly matching the dominant pattern of the distribution ranges as defined by their centroids (Fig. 2). The RSR, on the other hand, is more homogenous across Europe (Fig. 3(2)).

The comparison of overall fit of SDM for the 50 km × 50 km and 10 km × 10 km data showed significantly higher SM_{AUC} values (Wilcoxon test, $p < 0.001$) when models were run at finer spatial resolution. The improvement in model performance was also confirmed by a decrease in omission rates (Wilcoxon test, $p < 0.05$), ranging from 0.83 to 0.11 for the models at 50 km × 50 km and from 0.38 to 0.11 for those at 10 km × 10 km (Appendix A). The downscaled version (10 km × 10 km resolution) based on species ecology yielded an overall improvement of model performance, with 136 out of 147 species showing higher discriminatory power than at the original spatial resolution (i.e. at 50 km × 50 km). The downscaled SDM yielded an average increase in SM_{AUC} values of around 10%, although this increase was variable depending on the species modelled. By modelling at 10 km × 10 km resolution we also observed that the number of species with SM_{AUC} values below 0.75 was reduced from 92 (for the model at 50 km × 50 km) to 70 species.

The relatively low model performance for some species (i.e. below 0.75), even at 10 km × 10 km resolution, was highly influenced by the large number of occurrences (Fig. 4), which demonstrates the difficulties of developing SDM for common and widespread species. However, those species with AUC values below 0.75 at 10 km × 10 km showed a significantly better fit than expected by chance alone, as shown by the null models (Appendix A). Therefore, all 147 modelled species were used for our analysis.

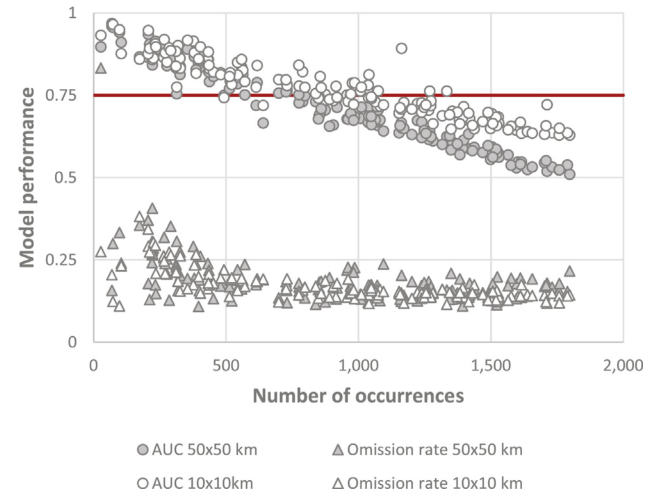

Fig. 4. Relationship between model performance (AUC and the omission rate) and the number of occurrences of the modelled species, at 50 km × 50 km and 10 km × 10 km spatial resolution. Values at 10 × 10 are the average of ten models run per species. AUC values above 0.75 (red line) were considered as good models (Elith, 2002). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Table 2
Non-parametric correlation analysis (Kendall's tau coefficient) between the distance to the dominant pattern of species distributions for the three groups of common birds (all common, farmland and forest birds) and both local and relative species richness respectively.

Functional group	Local species richness		Relative species richness	
	Mean *p*-value	tau coefficient	Mean *p*-value	tau coefficient
(1) Average values of 1000 random subsampling of 100 observations				
All common birds	<0.001	−0.41	0.301	−0.05
Farmland birds	<0.001	−0.36	0.302	−0.05
Forest birds	<0.001	−0.42	0.061	−0.16
(2) Average values of the variables at NUTS2 level				
All common birds	<0.001	−0.43	0.049	−0.07
Farmland birds	<0.001	−0.25	0.300	−0.02
Forest birds	<0.001	−0.52	0.036	−0.08

3.2. Spatial patterns of species richness

We found a very significant and strong negative correlation (i.e. tau coefficient) between the distance to the dominant pattern of species distributions and the LSR for all groups of common birds (Table 2). This indicates that higher species richness is found in areas where most species have their core distribution range (i.e. within the ellipses shown in Fig. 2). This significant negative correlation was consistent in both types of analyses performed, for the 1000 random subsamplings in the study area and for the correlation analysis at NUTS2 level (Table 2(1) and (2)).

In contrast, the correlation found between this distance and the RSR was in general non-significant (p-values >0.05) and/or with tau coefficients very close to 0. This shows that RSR follows a different spatial pattern than species richness, losing the strong relationship with the distance to the dominant pattern of species distributions. Only RSR for common forest birds showed a slight negative correlation for both types of analysis (random subsampling and NUTS2 level). However, the degree of correlation was reduced by about 70%

when comparing LSR with RSR (see the tau coefficients for common forest birds in Table 2(1) and (2)).

These results confirm the convenience of using RSR as a habitat quality indicator for common birds which is comparable between regions, since the influence of the dominant pattern of species distributions is practically eliminated for all species groups.

4. Discussion

In this study we presented a new habitat quality indicator developed for common birds in Europe using a species-based approach (i.e. by means of SDM). We demonstrated that the development of a HQI based on species richness needs to account for the variability in the regional species pool, as demonstrated by comparing the results obtained with the LSR and RSR. The HQI is built from an approach to downscale species occurrence data and the SDM derived thereof, grounded in an ecological basis. In contrast to other studies (Bombi and D'Amen, 2012), our method to refine species occurrences improved model performance, producing more accurate predictions of species distributions (as demonstrated by the increase in AUC values and decrease in omission rates). Importantly, the HQI for common birds here presented constitutes an innovative tool that may prove useful to support the assessment of the policy targets stated in the EU Biodiversity Strategy.

4.1. The habitat quality indicator for common birds

The results for modelled common birds in Europe clearly showed that habitat conditions for these species are not homogeneous everywhere. This indicates that the analysis of habitat suitability across large geographical extents is also very important for common species, even when they are thought to be evenly distributed.

This study proved that LSR for the target common birds was not a suitable proxy to compare regional habitat quality at the continental scale. This is especially important when the assessment of habitat quality is based on a given subset of target species (in our case, the common birds in Europe), rather than on the 'total' biodiversity (i.e. considering all or most species). Higher LSR was found in areas closer to the dominant pattern of the core distribution ranges, whereas RSR was able to compensate for this bias. This result confirms that, for common birds, lower LSR also reflects smaller regional species pools. In contrast, RSR compensated for the differences in the regional pools arising from the naturally heterogeneous patterns in the distribution ranges of the target species. Therefore, RSR, as defined in this study, was demonstrated to be an appropriate indicator of habitat quality to compare locations at the continental scale.

The influence of spatially heterogeneous patterns of species distributions on relative species richness was completely overcome for common farmland birds and all common birds. Only relative species richness for forest birds still presented nearly significant and significant correlation in the analysis at pixel and at NUTS2 level respectively, although with smaller correlation coefficients than for local species richness. This might be explained by the ellipses that measure the dominant pattern of species distributions, which show a higher dispersion of the species core ranges for farmland and all common birds than for common forest birds. Therefore, the results of this study suggest that the development of a habitat quality indicator based on a given pool of species should account for dispersion of the cores of species distribution ranges. This would reduce the large variability in the regional species pool that was found at continental scale and, therefore, contribute to obtaining a habitat quality indicator which is spatially congruent, with an appropriate representation across the (continent-wide) study area. The habitat quality indicator for common forest birds as presented here, however, can still be taken as a spatially coherent indicator, since the level of correlation was found to be very low.

4.2. Application to the EU Biodiversity targets

The use of relative species richness as a proxy of the HQI for common birds may have various applications within the context of the EU 2020 Biodiversity Strategy to measure progress towards the target of halting biodiversity loss in Europe. Our downscaled models at 10 km × 10 km are an added value to the SEBI 01 indicator (EEA, 2012), providing information about the distribution of selected species since distribution maps representing habitat suitability for common birds are not yet available. In this sense, the HQI could be used to identify areas where environmental measures might help increase the contribution of agriculture and forestry areas towards maintaining and enhancing biodiversity, as stated in Target 3 of the EU 2020 Biodiversity Strategy. A likely application would be an analysis of the overlap between the HQI for farmland birds and the High Natural Value farmland in Europe (Paracchini et al., 2008). Areas with high HQI for common farmland birds, but not considered as High Natural Value farmland, are those where the implementation of the agro-environmental measures of the Common Agriculture Policy might particularly favour populations of common farmland birds. This would contribute towards decreasing the threats for this group of species within potentially suitable areas, ultimately compensating for the negative trends in the populations of common farmland birds observed during the last decades (Inger et al., 2014).

The HQI based on SDM present important advantages such as the possibility to be projected on future land use or climate scenarios in order to assess potential changes. For instance, assessment of changes in the HQI under future land use scenarios simulating the implementation of different EU policies can be used to identify areas where land-use changes arising from different socio-economic drivers (Lopes Barbosa et al., 2015) are likely to affect habitat quality for common birds. An example of this projection to future scenarios is the contribution to Action 5 of the EU Biodiversity Strategy of Mapping and Assessment of Ecosystem Services (Maes et al., 2015). In this study, the HQI, based on SDM for breeding birds, is interpreted as a measure of the capacity of ecosystems to provide and maintain nursery/reproductive habitats for terrestrial species, one of the ecosystem services described in the Common International Classification of Ecosystem Services classification (Haines-Young and Potschin, 2013). In this sense, areas with better habitat quality are those providing suitable habitats for the reproduction of common birds in Europe.

However, for a correct application of the indicator it is important to bear in mind that the HQI based on SDM reflects the habitat suitability for target species at landscape scale based on the coexisting climate and land use conditions at 10 km × 10 km spatial resolution, consistent with the available maps (i.e. CLC). Therefore, this indicator does not provide information about the habitat quality regarding other types of environmental variables or at the local scale, which were not available to relate to the occurrence data across the whole study area.

Acknowledgements

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Appendix A.

List of common bird species and performance of species distribution models measured by AUC. Common bird species of the European Common birds indicator (European Bird Census Council, Species classification 2012) with AUC values and omission rates for species distribution models run at coarse (50 km × 50 km) and finer (10 km × 10 km) spatial resolution. Since models at 10 km × 10 km were run 10 independent times, the average and standard deviation of the AUC is also provided. For those models at 10 km × 10 km with AUC values below 0.75, the model performance of null models[a] is also given.

Group	Species name	Omission rate 50 km × 50 km	AUC 50 km × 50 km	Omission rate 10 km × 10 km Mean ± Stdv.	AUC 10 km × 10 km Mean ± Stdv.	AUC null models Mean ± Stdv.
Farmland	*Alauda arvensis*	0.151	0.577	0.146 ± 0.009	0.671 ± 0.005	0.498 ± 0.017
	Alectoris rufa	0.239	0.836	0.163 ± 0.031	0.858 ± 0.007	na
	Anthus campestris	0.175	0.750	0.220 ± 0.038	0.743 ± 0.008	0.506 ± 0.017
	Anthus pratensis	0.146	0.716	0.118 ± 0.014	0.813 ± 0.006	na
	Burhinus oedicnemus	0.275	0.814	0.156 ± 0.027	0.863 ± 0.008	na
	Calandrella brachydactyla	0.241	0.867	0.306 ± 0.045	0.868 ± 0.007	na
	Carduelis cannabina	0.210	0.584	0.151 ± 0.012	0.648 ± 0.008	0.501 ± 0.015
	Ciconia ciconia	0.135	0.749	0.168 ± 0.019	0.774 ± 0.006	na
	Corvus frugilegus	0.120	0.766	0.193 ± 0.029	0.780 ± 0.005	na
	Emberiza cirlus	0.188	0.794	0.190 ± 0.037	0.819 ± 0.008	na
	Emberiza citrinella	0.157	0.614	0.136 ± 0.018	0.716 ± 0.008	0.504 ± 0.013
	Emberiza hortulana	0.190	0.666	0.192 ± 0.020	0.720 ± 0.011	0.503 ± 0.021
	Emberiza melanocephala	0.240	0.911	0.232 ± 0.054	0.877 ± 0.009	na
	Falco tinnunculus	0.140	0.525	0.144 ± 0.011	0.640 ± 0.008	0.498 ± 0.016
	Galerida cristata	0.116	0.731	0.170 ± 0.026	0.755 ± 0.007	na
	Galerida theklae	0.333	0.942	0.110 ± 0.063	0.949 ± 0.009	na
	Hirundo rustica	0.155	0.524	0.141 ± 0.013	0.629 ± 0.006	0.504 ± 0.011
	Lanius collurio	0.139	0.669	0.150 ± 0.016	0.727 ± 0.009	0.505 ± 0.013
	Lanius minor	0.257	0.881	0.262 ± 0.025	0.865 ± 0.009	na
	Lanius senator	0.132	0.808	0.180 ± 0.025	0.821 ± 0.007	na
	Limosa limosa	0.253	0.840	0.207 ± 0.044	0.851 ± 0.013	na
	Melanocorypha calandra	0.370	0.865	0.344 ± 0.031	0.876 ± 0.009	na
	Miliaria calandra	0.228	0.677	0.192 ± 0.021	0.732 ± 0.009	0.512 ± 0.019
	Motacilla flava	0.150	0.612	0.151 ± 0.023	0.664 ± 0.009	0.497 ± 0.012
	Oenanthe hispanica	0.239	0.862	0.209 ± 0.035	0.879 ± 0.010	na
	Passer montanus	0.137	0.633	0.124 ± 0.014	0.696 ± 0.007	0.501 ± 0.010
	Perdix perdix	0.227	0.685	0.132 ± 0.016	0.788 ± 0.006	na
	Petronia petronia	0.128	0.887	0.274 ± 0.081	0.894 ± 0.008	na
	Saxicola rubetra	0.154	0.626	0.142 ± 0.021	0.718 ± 0.005	0.493 ± 0.014
	Saxicola torquata	0.213	0.675	0.159 ± 0.016	0.723 ± 0.009	0.497 ± 0.013
	Serinus serinus	0.238	0.642	0.154 ± 0.020	0.721 ± 0.008	0.503 ± 0.017
	Streptopelia turtur	0.142	0.649	0.119 ± 0.015	0.729 ± 0.005	0.501 ± 0.011
	Sturnus unicolor	0.175	0.914	0.294 ± 0.098	0.906 ± 0.014	na
	Sturnus vulgaris	0.159	0.593	0.127 ± 0.011	0.694 ± 0.004	0.506 ± 0.012
	Sylvia communis	0.130	0.627	0.152 ± 0.015	0.691 ± 0.009	0.494 ± 0.010
	Upupa epops	0.165	0.714	0.179 ± 0.018	0.744 ± 0.007	0.503 ± 0.016
	Vanellus vanellus	0.161	0.635	0.151 ± 0.011	0.721 ± 0.005	0.500 ± 0.010
Forest	*Accipiter nisus*	0.135	0.584	0.147 ± 0.017	0.675 ± 0.006	0.503 ± 0.009
	Anthus trivialis	0.131	0.609	0.157 ± 0.014	0.702 ± 0.008	0.493 ± 0.016
	Bombycilla garrulus	0.158	0.960	0.205 ± 0.072	0.969 ± 0.006	na
	Bonasa bonasia	0.193	0.789	0.184 ± 0.025	0.841 ± 0.003	na
	Carduelis spinus	0.168	0.727	0.154 ± 0.022	0.778 ± 0.007	na
	Certhia brachydactyla	0.182	0.689	0.164 ± 0.017	0.745 ± 0.005	0.503 ± 0.016
	Certhia familiaris	0.136	0.680	0.146 ± 0.019	0.763 ± 0.007	na
	Coccothraustes coccothraustes	0.219	0.679	0.137 ± 0.020	0.751 ± 0.006	na
	Columba oenas	0.160	0.679	0.134 ± 0.008	0.742 ± 0.006	0.486 ± 0.020
	Cyanopica cyanus	0.300	0.957	0.124 ± 0.044	0.965 ± 0.012	na
	Dendrocopos medius	0.162	0.786	0.164 ± 0.032	0.812 ± 0.009	na
	Dendrocopos minor	0.173	0.659	0.139 ± 0.011	0.716 ± 0.005	0.504 ± 0.013
	Dryocopus martius	0.160	0.670	0.136 ± 0.020	0.762 ± 0.007	na
	Emberiza rustica	0.179	0.935	0.292 ± 0.053	0.947 ± 0.004	na
	Ficedula albicollis	0.266	0.843	0.270 ± 0.034	0.859 ± 0.011	na
	Ficedula hypoleuca	0.132	0.733	0.138 ± 0.015	0.778 ± 0.005	na
	Garrulus glandarius	0.136	0.562	0.139 ± 0.013	0.666 ± 0.009	0.496 ± 0.011
	Nucifraga caryocatactes	0.109	0.846	0.200 ± 0.035	0.861 ± 0.006	na
	Parus ater	0.184	0.616	0.142 ± 0.010	0.705 ± 0.009	0.499 ± 0.014
	Parus cristatus	0.135	0.675	0.153 ± 0.019	0.730 ± 0.005	0.498 ± 0.015
	Parus montanus	0.151	0.706	0.144 ± 0.025	0.764 ± 0.010	na
	Parus palustris	0.174	0.687	0.145 ± 0.017	0.742 ± 0.008	0.512 ± 0.014
	Phoenicurus phoenicurus	0.150	0.602	0.139 ± 0.009	0.699 ± 0.007	0.500 ± 0.012
	Phylloscopus bonelli	0.236	0.833	0.217 ± 0.038	0.839 ± 0.006	na
	Phylloscopus collybita	0.159	0.601	0.160 ± 0.010	0.688 ± 0.008	0.504 ± 0.019
	Phylloscopus sibilatrix	0.164	0.695	0.150 ± 0.012	0.754 ± 0.008	na
	Picus canus	0.169	0.770	0.139 ± 0.035	0.807 ± 0.008	na
	Pyrrhula pyrrhula	0.203	0.651	0.145 ± 0.011	0.893 ± 0.008	na
	Regulus ignicapillus	0.236	0.752	0.170 ± 0.024	0.792 ± 0.005	na
	Regulus regulus	0.172	0.660	0.157 ± 0.011	0.740 ± 0.006	0.501 ± 0.012
	Sitta europaea	0.170	0.624	0.137 ± 0.016	0.733 ± 0.007	0.496 ± 0.012
	Tringa ochropus	0.180	0.859	0.181 ± 0.025	0.882 ± 0.009	na
	Turdus viscivorus	0.193	0.570	0.151 ± 0.012	0.664 ± 0.004	0.496 ± 0.012

Other	*Acrocephalus arundinaceus*	0.144	0.731	0.159 ± 0.017	0.821 ± 0.007	na
	Acrocephalus palustris	0.158	0.762	0.172 ± 0.015	0.784 ± 0.007	na
	Acrocephalus schoenobaenus	0.122	0.706	0.187 ± 0.021	0.753 ± 0.007	na
	Acrocephalus scirpaceus	0.147	0.682	0.141 ± 0.019	0.787 ± 0.008	na
	Actitis hypoleucos	0.169	0.660	0.170 ± 0.018	0.734 ± 0.009	0.497 ± 0.021
	Aegithalos caudatus	0.110	0.606	0.165 ± 0.014	0.673 ± 0.007	0.493 ± 0.013
	Anas platyrhynchos	0.180	0.519	0.119 ± 0.010	0.722 ± 0.007	0.499 ± 0.009
	Apus apus	0.178	0.530	0.132 ± 0.019	0.644 ± 0.011	0.491 ± 0.011
	Ardea cinerea	0.154	0.695	0.140 ± 0.031	0.807 ± 0.007	na
	Buteo buteo	0.199	0.579	0.124 ± 0.018	0.675 ± 0.009	0.498 ± 0.012
	Carduelis carduelis	0.179	0.588	0.144 ± 0.018	0.679 ± 0.009	0.510 ± 0.016
	Carduelis flammea	0.182	0.813	0.188 ± 0.027	0.826 ± 0.008	na
	Carpodacus erythrinus	0.194	0.868	0.235 ± 0.058	0.880 ± 0.007	na
	Cettia cetti	0.202	0.838	0.263 ± 0.066	0.832 ± 0.009	na
	Chloris chloris	0.139	0.548	0.139 ± 0.016	0.658 ± 0.005	0.498 ± 0.016
	Circus aeruginosus	0.135	0.757	0.123 ± 0.016	0.798 ± 0.007	na
	Cisticola juncidis	0.407	0.881	0.279 ± 0.078	0.899 ± 0.008	na
	Columba palumbus	0.194	0.538	0.140 ± 0.014	0.656 ± 0.007	0.502 ± 0.018
	Corvus corax	0.151	0.589	0.133 ± 0.010	0.682 ± 0.008	0.501 ± 0.020
	Corvus corone	0.172	0.569	0.128 ± 0.012	0.645 ± 0.006	0.505 ± 0.011
	Corvus monedula	0.162	0.592	0.174 ± 0.010	0.648 ± 0.005	0.508 ± 0.013
	Cuculus canorus	0.163	0.556	0.143 ± 0.018	0.649 ± 0.009	0.505 ± 0.012
	Cygnus olor	0.179	0.753	0.144 ± 0.024	0.842 ± 0.006	na
	Delichon urbica	0.216	0.510	0.144 ± 0.013	0.629 ± 0.012	0.501 ± 0.014
	Dendrocopos major	0.149	0.575	0.131 ± 0.010	0.685 ± 0.005	0.496 ± 0.015
	Emberiza cia	0.187	0.792	0.175 ± 0.029	0.830 ± 0.009	na
	Emberiza schoeniclus	0.125	0.674	0.152 ± 0.011	0.725 ± 0.006	0.497 ± 0.012
	Erithacus rubecula	0.136	0.547	0.175 ± 0.011	0.634 ± 0.008	0.501 ± 0.015
	Fringilla coelebs	0.167	0.532	0.148 ± 0.013	0.636 ± 0.004	0.496 ± 0.011
	Fringilla montifringilla	0.291	0.885	0.175 ± 0.022	0.915 ± 0.004	na
	Fulica atra	0.136	0.641	0.149 ± 0.012	0.763 ± 0.003	na
	Gallinago gallinago	0.185	0.709	0.148 ± 0.018	0.774 ± 0.006	na
	Gallinula chloropus	0.159	0.625	0.116 ± 0.009	0.763 ± 0.008	na
	Hippolais icterina	0.184	0.760	0.163 ± 0.025	0.797 ± 0.007	na
	Hippolais polyglotta	0.189	0.833	0.157 ± 0.028	0.856 ± 0.007	na
	Jynx torquilla	0.149	0.636	0.154 ± 0.018	0.696 ± 0.006	0.501 ± 0.011
	Locustella fluviatilis	0.286	0.874	0.304 ± 0.057	0.863 ± 0.012	na
	Locustella naevia	0.170	0.819	0.195 ± 0.023	0.813 ± 0.006	na
	Lullula arborea	0.197	0.656	0.136 ± 0.014	0.737 ± 0.006	0.489 ± 0.024
	Luscinia luscinia	0.157	0.888	0.185 ± 0.029	0.901 ± 0.008	na
	Luscinia megarhynchos	0.171	0.693	0.147 ± 0.016	0.751 ± 0.009	na
	Luscinia svecica	0.307	0.755	0.218 ± 0.060	0.775 ± 0.012	na
	Merops apiaster	0.126	0.796	0.196 ± 0.028	0.783 ± 0.009	na
	Motacilla alba	0.193	0.533	0.142 ± 0.019	0.636 ± 0.006	0.496 ± 0.016
	Motacilla cinerea	0.122	0.668	0.157 ± 0.019	0.781 ± 0.007	na
	Muscicapa striata	0.114	0.575	0.157 ± 0.014	0.659 ± 0.005	0.502 ± 0.013
	Numenius phaeopus	0.319	0.907	0.247 ± 0.045	0.920 ± 0.007	na
	Oenanthe oenanthe	0.155	0.582	0.150 ± 0.018	0.659 ± 0.009	0.500 ± 0.012
	Oriolus oriolus	0.126	0.676	0.160 ± 0.017	0.717 ± 0.007	0.496 ± 0.018
	Parus caeruleus	0.196	0.541	0.141 ± 0.020	0.668 ± 0.008	0.500 ± 0.011
	Parus major	0.154	0.538	0.141 ± 0.014	0.636 ± 0.007	0.502 ± 0.008
	Passer domesticus	0.170	0.546	0.142 ± 0.013	0.632 ± 0.009	0.498 ± 0.016
	Phoenicurus ochruros	0.124	0.667	0.150 ± 0.023	0.708 ± 0.004	0.505 ± 0.016
	Phylloscopus trochilus	0.833	0.898	0.275 ± 0.109	0.933 ± 0.016	na
	Pica pica	0.178	0.524	0.120 ± 0.015	0.650 ± 0.005	0.496 ± 0.008
	Picus viridis	0.185	0.631	0.134 ± 0.020	0.708 ± 0.010	0.504 ± 0.017
	Pluvialis apricaria	0.262	0.875	0.149 ± 0.032	0.897 ± 0.005	na
	Prunella modularis	0.172	0.622	0.134 ± 0.019	0.699 ± 0.004	0.499 ± 0.016
	Ptyonoprogne rupestris	0.219	0.821	0.207 ± 0.032	0.842 ± 0.007	na
	Pyrrhocorax pyrrhocorax	0.130	0.905	0.275 ± 0.060	0.893 ± 0.010	na
	Streptopelia decaocto	0.181	0.643	0.136 ± 0.013	0.714 ± 0.006	0.502 ± 0.017
	Sylvia atricapilla	0.138	0.587	0.129 ± 0.012	0.684 ± 0.006	0.503 ± 0.013
	Sylvia borin	0.131	0.659	0.146 ± 0.020	0.713 ± 0.007	0.505 ± 0.016
	Sylvia cantillans	0.229	0.875	0.213 ± 0.064	0.883 ± 0.016	na
	Sylvia curruca	0.175	0.686	0.165 ± 0.020	0.745 ± 0.006	0.500 ± 0.014
	Sylvia hortensis	0.356	0.867	0.382 ± 0.046	0.860 ± 0.013	na
	Sylvia melanocephala	0.352	0.864	0.266 ± 0.039	0.886 ± 0.008	na
	Sylvia nisoria	0.236	0.828	0.267 ± 0.047	0.817 ± 0.009	na
	Sylvia undata	0.148	0.889	0.210 ± 0.059	0.897 ± 0.009	na
	Tetrao tetrix	0.220	0.805	0.157 ± 0.027	0.850 ± 0.008	na
	Tringa glareola	0.194	0.890	0.163 ± 0.024	0.917 ± 0.003	na
	Tringa totanus	0.175	0.719	0.187 ± 0.023	0.775 ± 0.013	na
	Troglodytes troglodytes	0.177	0.562	0.155 ± 0.019	0.664 ± 0.007	0.501 ± 0.010
	Turdus iliacus	0.162	0.836	0.195 ± 0.018	0.859 ± 0.004	na
	Turdus merula	0.174	0.552	0.124 ± 0.016	0.658 ± 0.007	0.508 ± 0.015
	Turdus philomelos	0.137	0.598	0.128 ± 0.013	0.698 ± 0.006	0.492 ± 0.015
	Turdus pilaris	0.131	0.714	0.146 ± 0.016	0.775 ± 0.006	na

[a] Null models are used to assess the performance of models built from presence-only data, since these last models can only achieve a maximum AUC lower than one. In null models species occurrences are replaced by an equivalent number of randomly sampled locations (Raes and ter Steege, 2007). Null model performances were found to be significantly lower (Student's *t*-test <0.05) than the average AUC at 10 km × 10 km, indicating that distribution models built from occurrence data had significantly better fit than expected by chance alone. So, all species were included in the analysis.

Appendix B.

Since the IUCN habitat classification does not describe species preferences for heterogeneous habitats such as agriculture mixed with semi-natural vegetation and agro-forestry areas, included in CLC, we assumed that those species breeding in both arable land and shrublands will also show a preference for agriculture mixed with semi-natural vegetation, while those breeding in arable land and forests will show preferences for agro-forestry areas.

Correspondence between IUCN habitats and Corine Land Cover (CLC) classes.

IUCN habitat classification scheme[a]			CLC level	CLC classes
1	Forest		2	Forests
3	Shrubland		3	Moors and heathland, sclerophyllous vegetation, transitional woodland-shrub, burned areas
4	Grassland		3	Natural grasslands
5	Wetland			
	5.1.	Permanent Rivers, Streams, creeks	3	Water courses
	5.2.	Seasonal/Intermittent/Irregular Rivers, Streams, Creeks	3	
	5.3.	Shrub Dominated Wetlands	2	Inland wetlands
	5.4.	Bogs, Marshes, Swamps, Fens, Peatlands	2	
	5.5.	Permanent Freshwater Lake	3	Water bodies
	5.6.	Seasonal/Intermittent Freshwater Lakes	3	
	5.7.	Permanent Freshwater Marshes/Pools	2	Inland wetlands
	5.8.	Seasonal/Intermittent Freshwater Marshes/Pools	2	
	5.9.	Freshwater Springs and Oase	2	
	5.10.	Tundra Wetland	2	
	5.11.	Alpine Wetland	2	
	5.12.	Geothermal Wetland	2	
	5.13.	Permanent Inland Delta	2	
	5.14.	Permanent Saline, Brackish or Alkaline Lakes	2	
	5.15.	Seasonal/Intermittent Saline, Brackish or Alkaline Lakes	2	
	5.16.	Permanent Saline, Brackish or Alkaline Marshes/Pool	2	
	5.17.	Seasonal/Intermittent Saline, Brackish or Alkaline Marshes/Pool	2	
6	Rocky areas		3	Bare rocks, sparsely vegetated areas
9.10.	Estuaries		3	Estuaries
12	Marine intertidal			
	12.1.	Rocky Shoreline	3	Bare rocks
	12.2.	Sandy Shorelines and/or Beaches, Sand Bars, Spits	3	Beaches, dunes, sands
	12.3.	Shingle and/or Pebble Shoreline and/or Beaches	3	
	12.4.	Mud Shoreline and Intertidal Mud Flats	3	Intertidal flats
	12.5.	Salt Marshes (Emergent Grasses)	3	Salt marshes and salines
	12.6.	Tidepool	3	Coastal lagoons
13	Marine coastal/supratidal			
	13.1.	Sea Cliffs and Rocky Offshore Islands	3	Bare rocks
	13.3.	Coastal Sand Dunes	3	Beaches, dunes, sands
	13.4.	Coastal Brackish/Saline Lagoons/Marine Lake	2	Maritime wetlands
	13.5.	Coastal Freshwater Lakes	3	Water bodies
14	Terrestrial/artificial			
	14.1.	Arable land	3	Non-irrigated arable land, permanently irrigated land
	14.2.	Pastureland	3	Pastures
	14.3.	Plantations	2	Permanent crops
	14.4.	Rural gardens	3	Green urban areas
	14.5.	Urban areas	2	Urban fabric
15	Aquatic/artificial			
	15.7.	Irrigated land	3	Rice fields
	15.8.	Seasonal flooded agricultural land	3	

[a] Only those habitats of the IUCN identified as suitable for breeding birds are included in this table except the IUCN habitats related to artificial aquatic (ponds, wastewater treatment areas, canals. . .) which had not any likely correspondence in CLC classification.
Sources for habitats and land-use descriptions: http://www.iucnredlist.org/documents/Dec_2012_Guidance_Habitats_Classification_Scheme.pdf, http://sia.eionet.europa.eu/CLC2000/classes.

Appendix C.

Aggregation of the Corine Land Cover classes. Aggregation of the Corine Land Cover classes into the land use classes used in the species distribution models (SDM) as predictor variables.

Corine land use classes (label 3)	Land use classes SDM
Continuous urban fabric Discontinuous urban fabric Industrial or commercial units Road and rail networks and associated land Port areas Airports Mineral extraction sites Dump sites Construction sites Green urban areas Sport and leisure facilities	Artificial
Non-irrigated arable land Permanently irrigated land Rice fields	Arable
Vineyards Fruit trees and berry plantations Olive groves	Permanent crops
Pastures	Pastures
Annual crops associated with permanent crops Complex cultivation patterns Land principally occupied by agriculture, with significant areas of natural vegetation	Arable
Agro-forestry areas	Permanent crops
Broad-leaved forest Coniferous forest Mixed forest	Forests
Natural grasslands Moors and heathland Sclerophyllous vegetation	Natural land
Transitional woodland-shrub	Transitional woodland-shrub
Beaches, dunes, sands Bare rocks Sparsely vegetated areas Burnt areas Glaciers and perpetual snow	Other nature
Inland marshes Peat bogs Salt marshes Salines Intertidal flats	Wetlands
Water courses Water bodies Coastal lagoons Estuaries Sea and ocean	Water bodies

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